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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bazan, J. Fernando

(ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
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(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 24-JUL-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/053,765
(B) FILING DATE: 25-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0758K1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..567

Sequence Listing filed in USSN 09/122,443
For Reissue Application for Patent 6,060,284

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 64..567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CTG GGG AGC AGA GCT GTA ATG CTG CTG TTG CTG CTG CCC TGG ACA	48
Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Pro Trp Thr	
-21 -20	-15
	-10
GCT CAG GGC AGA GCT GTG CCT GGG GGC AGC AGC CCT GCC TGG ACT CAG	96
Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln	
-5	1
	5
	10
TGC CAG CAG CTT TCA CAG AAG CTC TGC ACA CTG GCC TGG AGT GCA CAT	144
Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His	
15	20
	25
CCA CTA GTG GGA CAC ATG GAT CTA AGA GAA GAG GGA GAT GAA GAG ACT	192
Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr	
30	35
	40
ACA AAT GAT GTT CCC CAT ATC CAG TGT GGA GAT GGC TGT GAC CCC CAA	240
Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln	
45	50
	55
GGA CTC AGG GAC AAC AGT CAG TTC TGC TTG CAA AGG ATC CAC CAG GGT	288
Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly	
60	65
	70
	75
CTG ATT TTT TAT GAG AAG CTG CTA GGA TCG GAT ATT TTC ACA GGG GAG	336
Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu	
80	85
	90
CCT TCT CTG CTC CCT GAT AGC CCT GTG GCG CAG CTT CAT GCC TCC CTA	384
Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu	
95	100
	105
CTG GGC CTC AGC CAA CTC CTG CAG CCT GAG GGT CAC CAC TGG GAG ACT	432
Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr	
110	115
	120
CAG CAG ATT CCA AGC CTC AGT CCC AGC CAG CCA TGG CAG CGT CTC CTT	480
Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu	
125	130
	135
CTC CGC TTC AAA ATC CTT CGC AGC CTC CAG GCC TTT GTG GCT GTA GCC	528
Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala	
140	145
	150
	155
GCC CGG GTC TTT GCC CAT GGA GCA GCA ACC CTG AGT CCC TAA	570
Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro	
160	165

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Pro Trp Thr
-21 -20 -15 -10

Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
-5 1 5 10

Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
15 20 25

Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
30 35 40

Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
45 50 55

Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
60 65 70 75

Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
80 85 90

Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
95 100 105

Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
110 115 120

Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
125 130 135

Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
140 145 150 155

Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
160 165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 113..700

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 176..700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCTTAGAAC	TCGGACTACA	GAGTTAGACT	CAGAACAAA	GGAGGTGGAT	AGGGGGTCCA	60	
CAGGCCTGGT	GCAGATCACA	GAGCCAGCCA	GATCTGAGAA	GCAGGGAACA	AG ATG	115	
					Met		
					-21		
CTG GAT TGC	AGA GCA	GTA ATA	ATG CTA	TGG CTG	TTG CCC TGG GTC	ACT	163
Leu Asp Cys	Arg Ala	Val Ile	Met Leu	Trp Leu	Leu Pro	Trp Val Thr	
-20	-15			-10		-5	
CAG GGC CTG GCT	GTG CCT AGG	AGT AGC	AGT CCT GAC	TGG GCT	CAG TGC	211	
Gln Gly Leu	Ala Val Pro	Arg Ser Ser	Pro Asp Trp	Ala Gln	Cys		
1	5			10			
CAG CAG CTC TCT	CGG AAT CTC	TGC ATG	CTA GCC	TGG AAC	GCA CAT GCA	259	
Gln Gln Leu	Ser Arg Asn	Leu Cys	Met Leu	Ala Trp	Asn Ala His Ala		
15	20			25			
CCA GCG GGA CAT	ATG AAT CTA	CTA AGA	GAA GAA	GAG GAT	GAA GAG ACT	307	
Pro Ala Gly His	Met Asn Leu	Leu Arg	Glu Glu	Asp Glu	Glu Thr		
30	35			40			
AAA AAT AAT GTG CCC CGT	ATC CAG TGT	GAA GAT	GGT TGT	GAC CCA	CAA 355		
Lys Asn Asn Val	Pro Arg Ile	Gln Cys	Glu Asp	Gly Cys	Asp Pro Gln		
45	50			55	60		
GGA CTC AAG GAC AAC	AGC CAG TTC	TGC TTG	CAA AGG ATC	CGC CAA	GGT 403		
Gly Leu Lys Asp	Asn Ser Gln	Phe Cys	Leu Gln	Arg Ile	Arg Gln Gly		
65	70			75			
CTG GCT TTT TAT	AAG CAC CTG CTT	GAC TCT	GAC ATC	TTC AAA	GGG GAG 451		
Leu Ala Phe Tyr	Lys His Leu	Leu Asp Ser	Asp Ile	Phe Lys	Gly Glu		
80	85			90			
CCT GCT CTA CTC	CCT GAT AGC CCC	ATG GAG CAA	CTT CAC ACC	TCC CTA	499		
Pro Ala Leu	Leu Pro Asp Ser	Pro Met	Glu Gln	Leu His	Thr Ser Leu		
95	100			105			
CTA GGA CTC AGC CAA	CTC CTC CAG CCA	GAG GAT CAC CCC	CGG GAG ACC		547		
Leu Gly Leu	Ser Gln Leu	Leu Gln Pro	Glu Asp His	Pro Arg Glu Thr			
110	115			120			
CAA CAG ATG CCC AGC	CTG AGT TCT	AGT CAG CAG	TGG CAG CGC CCC	CTT	595		
Gln Gln Met Pro Ser	Leu Ser Ser	Gln Gln Trp	Gln Arg Pro	Leu			
125	130			135	140		
CTC CGT TCC AAG ATC	CTT CGA AGC CTC	CAG GCC TTT	TTG GCC ATA	GCT	643		
Leu Arg Ser Lys	Ile Leu Arg Ser	Leu Gln Ala	Phe Leu Ala	Ile Ala			

145	150	155	
GCC CGG GTC TTT GCC CAC GGA GCA GCA ACT CTG ACT GAG CCC TTA GTG Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val 160	165	170	691
CCA ACA GCT TAAGGATGCC CAGGTTCCCA TGGCTACCAT GATAAGACTA Pro Thr Ala 175			740
ATCTATCAGC CCAGACATCT ACCAGTTAAT TAACCCATTA GGACTTGTGC TGTTCTTGT TCGTTTGTGTT TCGGTGAAGG GCAAGGACAC CATTATTAAA GAGAAAAGAA ACAAACCCCA GAGCAGGCAG CTGGCTAGAG AAAGGAGCTG GAGAAGAAGA ATAAAGTCTC GAGCCCTTGG CCTTGGAAAGC GGGCAAGCAG CTGCGTGGCC TGAGGGGAAG GGGGCGGTGG CATCGAGAAA CTGTGAGAAA ACCCAGAGCA TCAGAAAAAG TGAGCCCAGG CTTTGGCCAT TATCTGTAAG AAAAACAAGA AAAGGGGAAC ATTATACTTT CCTGGGTGGC TCAGGGAAAT GTGCAGATGC ACAGTACTCC AGACAGCAGC TCTGTACCTG CCTGCTCTGT CCCTCAGTTC TAACAGAATC TAGTCACTAA GAACTAACAG GACTACCAAT ACGAACGTGAC AAA			800 860 920 980 1040 1100 1160 1203

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val
-21 -20 -15 -10

Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln
-5 1 5 10

Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His
15 20 25

Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Asp Glu Glu
30 35 40

Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
45 50 55

Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln
60 65 70 75

Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
80 85 90

Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
95 100 105

Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
110 115 120

Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
125 130 135

Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
140 145 150 155

Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
160 165 170

Val Pro Thr Ala
175

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu
1 5 10 15

Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
20 25 30

Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
35 40 45

Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
50 55 60

Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
65 70 75 80

Ser Leu Gln Ala Phe Val Ala Val Ala Arg Val Phe Ala His Gly
85 90 95

Ala Ala Thr Leu Ser Gln
100

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Pro Leu Gly Pro Ala Arg Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Ala Asp Gly Ala Glu Leu Gln
20 25 30

Glu Arg Leu Cys Ala Ala His Lys Leu Cys His Pro Glu Glu Leu Met
35 40 45

Leu Leu Arg His Ser Leu Gly Ile Pro Gln Ala Pro Leu Ser Ser Cys
50 55 60

Ser Ser Gln Ser Leu Gln Leu Arg Gly Cys Leu Asn Gln, Leu His Gly
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Ala Gly Ile Ser
85 90 95

Pro Glu Leu Ala Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Thr Asp
100 105 110

Phe Ala Thr Asn Ile Trp Leu Gln Met Glu Asp Leu Gly Ala Ala Pro
115 120 125

Ala Val Gln Pro Thr Gln Gly Ala Met Pro Thr Phe Thr Ser Ala Phe
130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser Gln Leu His Arg Phe
145 150 155 160

Leu Glu Leu Ala Tyr Arg Gly Leu Arg Tyr Leu Ala Glu Pro
165 170

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Pro Leu Gly Pro Thr Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Cys Leu Glu Gln Val Arg Lys Val Gln Ala Asp Gly Thr Ala Leu Gln
20 25 30

Glu Arg Leu Cys Ala Ala His Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45

Leu Leu Gly His Ala Leu Gly Ile Pro Gln Ala Pro Leu Ser Ser Cys
50 55 60

Ser Ser Gln Ala Leu Gln Leu Thr Gly Cys Leu Arg Gln Leu His Ser
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Ala Gly Ile Ser
85 90 95

Pro Glu Leu Ala Pro Thr Leu Asp Met Leu Gln Leu Asp Ile Thr Asp
100 105 110

Phe Ala Ile Asn Ile Trp Gln Gln Met Glu Asp Val Gly Met Ala Pro
115 120 125

Ala Val Pro Pro Thr Gln Gly Thr Met Pro Thr Phe Thr Ser Ala Phe
130 135 140

Gln Arg Arg Ala Gly Gly Thr Leu Val Ala Ser Asn Leu Gln Ser Phe
145 150 155 160

Leu Glu Val Ala Tyr Arg Ala Leu Arg His Phe Thr Lys Pro
165 170

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30

Glu Lys Leu Val Ser Glu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
35 40 45

Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
50 55 60

Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln
65 70 75 80

Leu His Ser Gly Leu Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
85 90 95

Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu
100 105 110

Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
115 120 125

Arg His Leu Ala Gln Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
130 135 140

Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
145 150 155 160

Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
165 170 175

Pro

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Pro Leu Val Thr Val Ser Ala Leu Pro Pro Ser Leu Pro Leu Pro
1 5 10 15

Arg Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Ala
20 25 30

Ser Gly Ser Val Leu Leu Glu Gln Leu Cys Ala Thr Tyr Lys Leu Cys
35 40 45

His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Lys
50 55 60

Ala Ser Leu Ser Gly Cys Ser Ser Gln Ala Leu Gln Gln Thr Gln Cys
65 70 75 80

Leu Ser Gln Leu His Ser Gly Leu Cys Leu Tyr Gln Gly Leu Leu Gln
85 90 95

Ala Leu Ser Gly Ile Ser Pro Ala Leu Ala Pro Thr Leu Asp Leu Leu
100 105 110

Gln Leu Asp Val Ala Asn Phe Ala Thr Thr Ile Trp Gln Gln Met Glu
115 120 125

Asn Leu Gly Val Ala Pro Thr Val Gln Pro Thr Gln Ser Ala Met Pro
130 135 140

Ala Phe Thr Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Ala Ile
145 150 155 160

Ser Tyr Leu Gln Gly Phe Leu Glu Thr Ala Arg Leu Ala Leu His His
165 170 175

Leu Ala

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ser Lys Asp Asp Ala
1 5 10 15

Thr Ser Asn Arg Pro Pro Leu Thr Ser Ala Asp Lys Met Glu Asp Phe
20 25 30

Ile Lys Phe Ile Leu Gly Lys Ile Ser Ala Leu Arg Asn Glu Met Cys
35 40 45

Asp Lys Tyr Asn Lys Cys Glu Asp Ser Lys Glu Val Leu Ala Glu Asn
50 55 60

Asn Leu Asn Leu Pro Lys Leu Ala Glu Lys Asp Arg Cys Phe Gln Ser
65 70 75 80

Arg Phe Asn Gln Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln
85 90 95

Glu Phe Gln Ile His Leu Lys Tyr Leu Glu Ser Asn Tyr Glu Gly Asn
100 105 110

Lys Asp Asn Ala His Ser Val Tyr Ile Ser Thr Lys His Leu Leu Gln

115

120

125

Thr Leu Arg Pro Met Asn Gln Ile Glu Val Thr Thr Pro Asp Pro Thr
 130 135 140

Thr Asp Ala Ser Leu Gln Ala Leu Phe Lys Ser Gln Asp Lys Trp Leu
 145 150 155 160

Lys His Thr Thr Ile His Leu Ile Leu Arg Arg Leu Glu Asp Phe Leu
 165 170 175

Gln Phe Ser Leu Arg Ala Ile Arg Ile Met
 180 185

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ala Thr Ser Asn Arg
 1 5 10 15

Leu Pro Leu Thr Pro Ala Asp Lys Met Glu Glu Leu Ile Lys Tyr Ile
 20 25 30

Leu Gly Lys Ile Ser Ala Leu Lys Lys Glu Met Cys Asp Asn Tyr Asn
 35 40 45

Lys Cys Glu Asp Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu
 50 55 60

Pro Lys Leu Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Gln
 65 70 75 80

Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln Glu Phe Gln Ile
 85 90 95

Tyr Leu Lys Phe Leu Gln Asp Lys Tyr Glu Gly Asp Lys Glu Asn Ala
 100 105 110

Lys Ser Val Tyr Thr Ser Thr Asn Val Leu Leu Gln Met Leu Lys Arg
 115 120 125

Lys Gly Lys Asn Gln Asp Glu Val Thr Ile Pro Val Pro Thr Val Glu
 130 135 140

Val Gly Leu Gln Leu Ser Cys Ser His Arg Arg Val Ala Glu Ala His
 145 150 155 160

Asn Asn His Leu Thr Leu Arg Arg Leu Glu Asp Phe Leu Gln Leu Arg
165 170 175

Leu Arg Ala Val Arg Ile Met
180

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Phe Pro Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
1 5 10 15

Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln
20 25 30

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys
35 40 45

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn
50 55 60

Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser
65 70 75 80

Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu
85 90 95

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser
100 105 110

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln
115 120 125

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp
130 135 140

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln
145 150 155 160

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
165 170 175

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
180 185

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Phe	Pro	Thr	Pro	Gly	Pro	Leu	Gly	Glu	Asp	Phe	Lys	Asn	Asp	Thr
1					5				10						15
Thr	Pro	Ser	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Glu	Lys	Thr	Glu	Ala	Leu
				20				25						30	
Ile	Lys	His	Ile	Val	Asp	Lys	Ile	Ser	Ala	Ile	Arg	Lys	Glu	Ile	Cys
	35					40						45			
Glu	Lys	Asn	Asp	Glu	Cys	Glu	Asn	Ser	Lys	Glu	Thr	Leu	Ala	Glu	Asn
	50				55				60						
Lys	Leu	Lys	Leu	Pro	Lys	Met	Glu	Glu	Lys	Asp	Gly	Cys	Phe	Gln	Ser
	65				70				75					80	
Gly	Phe	Asn	Gln	Ala	Ile	Cys	Leu	Ile	Lys	Thr	Thr	Ala	Gly	Leu	Leu
				85				90					95		
Glu	Tyr	Gln	Ile	Tyr	Leu	Asp	Phe	Leu	Gln	Asn	Glu	Phe	Glu	Gly	Asn
				100				105				110			
Gln	Glu	Thr	Val	Met	Glu	Leu	Gln	Ser	Ser	Ile	Arg	Thr	Leu	Ile	Gln
				115				120				125			
Ile	Leu	Lys	Glu	Lys	Ile	Ala	Gly	Leu	Ile	Thr	Thr	Pro	Ala	Thr	His
		130				135			140						
Thr	Asp	Met	Leu	Glu	Lys	Met	Gln	Ser	Ser	Asn	Glu	Trp	Val	Lys	Asn
	145				150				155			160			
Ala	Lys	Val	Ile	Ile	Ile	Leu	Arg	Ser	Leu	Glu	Asn	Phe	Leu	Gln	Phe
				165				170				175			
Ser	Leu	Arg	Ala	Ile	Arg	Met	Lys								
				180											

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Phe Pro Thr Ser Gln Val Arg Arg Gly Asp Phe Thr Glu Asp Thr
1 5 10 15

Thr Pro Asn Arg Pro Val Tyr Thr Thr Ser Gln Val Gly Gly Leu Ile
20 25 30

Thr His Val Leu Trp Glu Ile Val Glu Met Arg Lys Glu Leu Cys Asn
35 40 45

Gly Asn Ser Asp Cys Met Asn Asn Asp Asp Ala Leu Ala Glu Asn Asn
50 55 60

Leu Lys Leu Pro Glu Ile Gln Arg Asn Asp Gly Cys Tyr Gln Thr Gly
65 70 75 80

Tyr Asn Gln Glu Ile Cys Leu Leu Lys Ile Ser Ser Gly Leu Leu Glu
85 90 95

Tyr His Ser Tyr Leu Glu Tyr Met Lys Asn Asn Leu Lys Asp Asn Lys
100 105 110

Lys Asp Lys Ala Arg Val Leu Gln Arg Asp Thr Glu Thr Leu Ile His
115 120 125

Ile Phe Asn Gln Glu Val Lys Asp Leu His Lys Ile Val Leu Pro Thr
130 135 140

Pro Ile Ser Asn Ala Leu Leu Thr Asp Lys Leu Glu Ser Gln Lys Glu
145 150 155 160

Trp Leu Arg Thr Lys Thr Ile Gln Phe Ile Leu Lys Ser Leu Glu Glu
165 170 175

Phe Leu Lys Val Thr Leu Arg Ser Thr Arg Gln Thr
180 185

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Pro Leu Ala Glu Leu Ser Gly Asp His Asp Phe Gln Leu Phe Leu
 1 5 10 15

His Lys Asn Leu Glu Phe Thr Arg Lys Ile Arg Gly Asp Val Ala Ala
 20 25 30

Leu Gln Arg Ala Val Cys Asp Thr Phe Gln Leu Cys Thr Glu Glu Glu
 35 40 45

Leu Gln Leu Val Gln Pro Asp Pro His Leu Val Gln Ala Pro Leu Asp
 50 55 60

Gln Cys His Lys Arg Gly Phe Gln Ala Glu Val Cys Phe Thr Gln Ile
 65 70 75 80

Arg Ala Gly Leu His Ala Tyr His Asp Ser Leu Gly Ala Val Leu Arg
 85 90 95

Leu Leu Pro Asn His Thr Thr Leu Val Glu Thr Leu Gln Leu Asp Ala
 100 105 110

Ala Asn Leu Ser Ser Asn Ile Gln Gln Met Glu Asp Leu Gly Leu
 115 120 125

Asp Thr Val Thr Leu Pro Ala Glu Gln Arg Ser Pro Pro Pro Thr Phe
 130 135 140

Ser Gly Pro Phe Gln Gln Gln Val Gly Gly Phe Phe Ile Leu Ala Asn
 145 150 155 160

Phe Gln Arg Phe Leu Glu Thr Ala Tyr Arg Ala Leu Arg His Leu Ala
 165 170 175

Arg Leu

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys Asp Leu Leu
 1 5 10 15

Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu Cys Phe Arg
 20 25 30

Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu Glu Pro Ala
35 40 45

Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr Asp His Cys
50 55 60

Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys Leu Ala Asp
65 70 75 80

Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr Thr Glu Phe
85 90 95

Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu Thr Lys Thr
100 105 110

Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr Lys Thr His
115 120 125

Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg Leu Gln Gly
130 135 140

Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val Leu Ser Ala
145 150 155 160

Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp Ser Ile Pro
165 170 175

Asp Val Thr Pro Asp Val His Asp Lys
180 185